

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 23, 2003, 12:29:01, Search time 2393 seconds
(without alignments)
15773.026 Million cell updates/sec

Title: US-09-745-506-74
Perfect score: 1553
Sequence: 1 GTCATTGTAATCTGCGCT.....TCGTCTTACTTAACATTCAA 1553

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_liv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pir:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vit:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1034	66.6	1201	9	AL529615
2	1014.2	65.3	1201	9	AL582089
3	1008.4	64.9	1201	9	AL563496
4	952.2	61.3	1117	12	BMS45164

Result No.	Score	Query Match	Length	ID	Description
5	933.2	60.1	1201	9	AL523985
6	931.6	60.0	1201	9	AL581997
7	931.6	60.0	1201	13	BX446370
8	924.6	59.5	1201	13	BX377118
9	861	55.4	930	13	BX393871
10	860	55.4	1006	13	BX386928
11	855.6	55.1	984	13	BX385101
12	855.2	55.1	1376	11	AK011670
13	850.2	54.7	929	13	BUS95307
14	850	54.7	929	13	BQ927763
15	847.4	54.6	961	9	AL521919
16	841.4	54.2	857	13	BQ172435
17	839.8	54.1	1201	13	BUS23986
18	828.4	53.3	919	13	BUS26538
19	827.6	53.3	957	9	AL521920
20	823.6	53.0	1079	13	BX393175
21	818	52.7	997	13	BX386927
22	793	51.1	1467	11	AK003978
23	792.2	51.0	836	13	BQ229243
24	782.4	50.4	886	9	AL520537
25	770.6	49.6	890	9	AL520538
26	765.4	49.3	877	13	BQ437698
27	750.6	48.3	1019	12	BMS57530
28	750.4	48.3	888	13	BQ195469
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30	732.6	47.2	817	12	B1755123
31	731	47.1	742	12	B1093955
32	728.4	46.9	811	10	BQ213848
33	725	46.7	796	9	AU134237
34	723.2	46.6	963	10	BE797115
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37	712	45.8	871	12	BG765986
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40	705.4	45.4	1032	12	BM810545
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42	701.6	45.2	859	10	BE975933
43	698.4	45.0	909	14	CD385139
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45	697.6	44.9	980	13	BQ854847

ALIGNMENTS

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LOCUS AL529615 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
DEFINITION CDNA clone CS0DD006YH18 5-PRIME, mRNA sequence.

ACCESSION AL529615
VERSION AL529615.2 GI:31067458
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced g1.12793108.

Contact: Genoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

1287.f For more information about this cluster, see

http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DD006D090p1ac1cluster=1287.f. Contact :

Feng Liang Email: fliang@lifetech.com URL:

Db	1168	SCCCMCAMATAMTAAATTTAAATTTCTCCKMGACATATGACCTACTGAGAGATGA-KRG	1110
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Qy	581	TGTTGGCTAAAGGCTTGAGCTTGTACTCCAGGCCCATACATCTTCCAAAGCTCC	640
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Db	32	ACCATATT	25
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LOCUS			
DEFINITION			
AL563496 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens			
CDNA clone CS0DD006YH18 3-PRIME, mRNA sequence.			
VERSION			
AL563496.2 GI:31287490			
KEYWORDS			
EST.			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
REFERENCE			
1 (bases 1 to 1201)			
AUTHORS			
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.			
TITLE			
Full-length cDNA libraries and normalization			
JOURNAL			
Unpublished			
COMMENT			
On Feb 15, 2001 this sequence version replaced gi:12912946.			
Contact: Genoscope			
Genoscope - Centre National de Sequencage			
BP 191 91006 Evry cedex - France			
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr			
was normalized. Library was constructed by Life Technologies, a			
division of Invitrogen. This sequence belongs to sequence cluster			
1287.f For more information about this cluster, see			
http://www.genoscope.cns.fr/			
cgl-bin/cluster.cgi?seq=CS0DD006YH18&cluster=1287.f. Contact :			
Peng Liang Email: fliang@life.com URL :			
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600			
Faraday Avenue Genoscope sequence ID : CS0DD006YH18.			
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sites of the pCMVSPORT 6 vector. Library was normalized."			
BASE COUNT			
325 a 268 c 278 g 298 t 32 others			
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Matches 1102; Conservative 22; Mismatches 74; Indels 6; Gaps 6;			
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Qy	444	CGCCATATCTTCCGA-CCCATGAGGCGATTAACCTGGAACACATGGAAGGCGCTGGG	502
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Qy	503	ATCCGGGCTGAGAGACAGAGTGGTATCTACTCTCCATACAGCCATGATGCTGCG	562
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 DB 662 GAAGACGGAATTTCTGTCTGAGAGAGCTTTGCTTCTACATCTGGAATGGAGCGTT 603
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 RESULT 4
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 ACCESSION BMS45164
 VERSION BMS45164.1 GI:18777026

KEYWORDS EST.
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 1117)
 NIH-MGC <http://mgi.mcl.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 UNPUBLISHED
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Invitrogen
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
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 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
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 QY 417 AGGACAGCTCATTTCTCTCTACATCCGCTATCTTCCGACCAATGAGGCTAATCCT 476
 DB 260 AGGACAGCTCATTTCTCTCTACATCCGCTATCTTCCGACCAATGAGGCTAATCCT 319
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RESULT 5
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 LOCUS AL523985 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
 DEFINITION cDNA clone CS0DC003YB10 3-PRIME, mRNA sequence.
 ACCESSION AL523985
 VERSION AL523985.2 GI:31042246
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1201)
 L1.W.B., Gruber,C., Jessee,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished
 On Feb 13, 2001 this sequence version replaced gi:12787478.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by life technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 1287.f for
 more information about this cluster, see
 http://www.genoscope.cns.fr/

cg1-bin/cluster.cg12seq-CS0DC003DA05NP1ecluster=1287.f. Contact :
 Feng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DC003DA05NP1.
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 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 323 a 249 c 273 g 320 t 36 others
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 Query Match 60.1%; Score 93.2; DB 9; Length 1201;
 Best Local Similarity 93.5%; Pred. No. 1.5e-241;
 Matches 1029; Conservative 18; Mismatches 42; Indels 11; Gaps 7;
 QY 416 AAGCAGACCTATCTCTCTCCATACCCGCTATCTCCGACCCATGAGCGATTAAC 475
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 QY 716 GCAAGTGAAGGAATTTGAGCGGTCTCTGCACTTCTTTTCTGCTAGAGCTGTATAGAG 775
 Db 809 GCAAGTGAAGGAATTTGAGCGGTCTCTGCACTTCTTTTCTGCTAGAGCTGTATAGAG 750
 QY 776 GAAACAAACGAGTGAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 835
 Db 749 GAAACAAACGAGTGAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 690
 QY 836 CTTCGCCGGAACAAACCTTTATGAGAAGAGGAAATTTCTGTMACTGTGAAGAGCTTTG 895
 Db 689 CTTCGCCGGAACAAACCTTTATGAGAAGAGGAAATTTCTGTMACTGTGAAGAGCTTTG 630
 QY 896 CTTCACATCTGGAATTTGAGCGGTCTTCTGACCTCTTTTTCGTAGACGTGTAAATGAG 955
 Db 629 CTTCACATCTGGAATTTGAGCGGTCTTCTGACCTCTTTTTCGTAGACGTGTAAATGAG 570
 QY 956 ATGATTTGATGGAATTAATAAGACACCTTAACATATCTCATATTCGCTTACGCCCTTGGG 1015
 Db 569 ATGATTTGATGGAATTAATAAGACACCTTAACATATCTCATATTCGCTTACGCCCTTGGG 510
 QY 1016 GGGAGAACCTTAGAGTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1075
 Db 509 GGGAGAACCTTAGAGTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 450
 QY 1076 GTTCTCAAGGCTTGAAGCTGTGACCTTACCTCAAGGCTGAGATGCTCCATCATGATACT 1135
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Db 389 TTGATGCTGCTCCAGAGAAATTAATGATCTCTGTGAACACAGCAACACTGACGA 330
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 QY 1256 ATCTATCTGAGACAGACAGGAGACCTCTTCAGAGTGTATTAATGCAAGAACATCAGAT 1315
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 QY 1316 AACACATCTCTCAATCAATGAGTGTATTCCTCACTTAAATTTGATACATAGTACAGAGGA 1375
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 QY 1376 CTGCTGTCTTCAGAGAGTGTCTTCAGAGGATATCATCTATTCCTGTTTGTATCTTAT 1435
 Db 151 CTGCTGTCTTCAGAGAGTGTCTTCAGAGGATATCATCTATTCCTGTTTGTATCTTAT 92
 QY 1436 TCACCAAAATGTTCTATCGCTCGTAAGTAAACTGTAATATACCTACCTATTAATTAAC 1495
 Db 91 TCACCAAAATGTTCTATGCTGTAAGTAAACTGTAATATACCTACCTATTAATTAAC 32
 QY 1496 AATGTTCTATTAATCTCT 1515
 Db 31 AATGTTCTATTAATCTCT 13

RESULT 6
 AL581997 1201 bp mRNA linear EST 01-JUN-2003
 LOCUS AL581997 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
 DEFINITION Homo sapiens cDNA clone CSDDL003Y624 5-PRIME, mRNA sequence.
 ACCESSION AL581997
 VERSION AL581997.2 GI:31320228
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 16, 2001 this sequence version replaced gi:12949550.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: sequef@genoscope.cns.fr Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 1287.f For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CSDDL003B120P1&cluster=1287.f Contact :
 Feng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CSDDL003B120P1.

FEATURES

source

1. 1201
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 /db_xref="taxon:9606"
 /clone="CSDDL003Y624"
 /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
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 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 293 a 286 c 277 g 310 t 35 others
 ORIGIN

Query Match 60.0%; Score 931.6; DB 9; Length 1201;
 Best Local Similarity 95.5%; Pred. No. 4.1e-241;
 Matches 991; Conservative 10; Mismatches 29; Indels 8; Gaps 4;
 QY 169 TGAATGAGGCAATAGATGATGCTCCACGACGAGCGGTTGATGATCCGTGATCGCA 228
 Db 97 TGTCACTCTGCGTACCCCACTCCACGACGAGCGGTTGATGATCCGTGATCGCA 156
 QY 229 TTCTTCCGTTCCCTTCATGATTTGAAGGCTCTCTTCTTCTTCTTGAATGATTTGATC 288
 Db 157 TTCTTCCGTTCCCTTCATGATTTGAAGGCTCTCTTCTTCTTCTTGAATGATTTGATC 216
 QY 289 CCTCTGTTTCTGAGAGTTGGGCAATGTTGATTTACTGTTGGAACCAAGCCACCA 348
 Db 217 CCTCTGTTTCTGAGAGTTGGGCAATGTTGATTTACTGTTGGAACCAAGCCACCA 276
 QY 349 TACTGTAATATACCTCTCTCTGACATGACCTGATGAGGAATGATGAGAGGTGCT 408
 Db 277 TACTGTAATATACCTCTCTCTGACATGACCTGATGAGGAATGATGAGAGGTGCT 336
 QY 409 GCAAAAGAGGAGACCTCATCTCTCTACCATCCGCTATCTTCCGACCATGAGAG 468
 Db 337 GCAAAAGAGGAGACCTCATCTCTCTACCATCCGCTATCTTCCGACCATGAGAG 396
 QY 469 CATACCTGAGACATGAGAGAGGCGCTGTGATCCGGCTCTGGAACAAGATCGG 528
 Db 397 CATACCTGAGACATGAGAGAGGCGCTGTGATCCGGCTCTGGAACAAGATCGG 456
 QY 529 TATCTACTCTCTCTCATACAGCCATGATGCTGCGCCACAGGCGCTCAACATGCTGGC 588
 Db 457 TATCTACTCTCTCTCATACAGCCATGATGCTGCGCCACAGGCGCTCAACATGCTGGC 516
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 QY 1068 GGAGCAGCGTTGCGAGGCGGTGAGGCTGACCTTACCTCAGAGGTGAGATGCCATC 1127
 Db 997 GGAGCAGCGTTGCGAGGCGGTGAGGCTGACCTTACCTCAGAGGTGAGATGCCATC 1054
 QY 1128 ATGATCTTGTGATGCTGCTCCAGAGATTAATGCTCATCTCTGATGAGACAGCA 1187
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Db 1110 CTGACGAGSTTTTCT 1127

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RESULT 7
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LOCUS BX446370 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBA0042B11
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX446370
VERSION BX446370.1 GI:31023721
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1287.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CLOBA0042B11&cluster=1287.f. Contact :
Feng Liang Email: fliang@life.techn.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CLOBA0042B11RP1.
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1. 1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CLOBA0042B11"
/issue_type="PLACENTA"
/note="Vector: PCWVSORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the PCWVSORT 5 vector.
Library was not normalized."
BASE COUNT 349 a 256 c 266 g 296 t 34 others
ORIGIN

Query Match 60.08; Score 931.6; DB 13; Length 1201;
Best Local Similarity 98.78; Pred. No. 4.1e-241;
Matches 965; Conservative 5; Mismatches 4; Indels 4; Gaps 3;

QY 386 GAGGAAGTATGAGGAGGCTGTCGAAGAAGCAGACCTTCCTCTTACCATCCG 445
DB 67 GATGAAATGATGAGGAGGCTGTCGAAGAAGCAGACCTTCCTCTTACCATCCG 126
QY 446 CCTATCTCCGACCATGAAGCGCATTAACCTGGAACACATGGAAGAGCGCTGTATC 505
DB 127 CCAATCTCCGACCATGAAGCGCATTAACCTGGAACACATGGAAGAGCGCTGTATC 186
QY 506 CGGCGCTTGAGAAACAGATGCTATCTCTCTCATACAGCCTATGAGTGCGCC 565
DB 187 CGGCGCTTGAGAAACAGATGCTATCTCTCTCATACAGCCTATGAGTGCGCC 246
QY 566 CAGGCGCTGAACAACCTGTTGGCTAAAGGCTTGAGCTGTACTCCAGGCCCATCAT 625
DB 247 CAGGCGCTGAACAACCTGTTGGCTAAAGGCTTGAGCTGTACTCCAGGCCCATCAT 306
QY 626 CTTTCCAAAGCTCCCACTACCTACAGAGGGAACACCGAGTAGAATTCAGGTTAAC 685
DB 307 CTTTCCAAAGCTCCCACTACCTACAGAGGGAACACCGAGTAGAATTCAGGTTAAC 366
QY 686 TACACCCAAAGCTGGAACAGTATCTGTGACGTGAAGAATTCAGCGGTTTCTGTC 745

Db 367 TACACCCAAAGCTGGAACAGTATCTGTGACGTGAAGAATTCAGCGGTTTCTGTC 426
QY 746 ACTTCTTTTCTGCTAGACCTGTAATGAGAAACAACACGATTAATCTAATTTCTACT 805
DB 427 ACTTCTTTTCTGCTAGACCTGTAATGAGAAACAACACGATTAATCTAATTTCTACT 486
QY 806 CAGAAGGCTTGATGACAGGTGTAATTTTCTTCCCGGAACAACACTTATCAGAA 865
DB 487 CAGAAGGCTTGATGACAGGTGTAATTTTCTTCCCGGAACAACACTTATCAGAA 546
QY 866 ACGGAATTTCTGCTAGCTGAGAACCTTTGCTTCTACATCTGAAATGGAAGCTTATGC 925
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DB 607 ACATGATGATGATGCTGCTCCCTGGAACACATGATGATGATGATGATGATGATGAT 666
QY 986 CTATCTCATATTCGCTTACAGCCCTTGGGGTGGGGAACCTTAGAGTCTCAAGTCAAGTGC 1045
DB 667 CTATCTCATATTCGCTTACAGCCCTTGGGGTGGGGAACCTTAGAGTCTCAAGTCAAGTGC 726
QY 1046 GTGGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1105
DB 727 GTGGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
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DB 787 CTCACAGGTGAGATGCTCCCATCATGATGATGATGATGATGATGATGATGATGATGAT 846
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RESULT 8
BX377118/c 1201 bp mRNA linear EST 08-MAY-2003
LOCUS BX377118 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSOD1002YH20 3-PRIME, mRNA sequence.
ACCESSION BX377118
VERSION BX377118.1 GI:30448573
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1287.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOD1002YH20&cluster=1287.f. Contact :

OY	153	AGGCGTGAAGTGGACACTGGAATATGAGGCATAGATAGTCCACAGACAGTCCGGTTTGTAG	212
Db	38	AGGCTGTATACCGGTCGGGAATTTCCCGGAGATGAGTATGCCACACAGATCCGGTTTGTAG	97
OY	213	ATTCCCTGATCTGTGAATTTCTTCCCGTTCCCTTCATGGAATTTGAAGGCTCTCTTCTTCTCT	272
Db	98	ATTCCCTGATCTGTGAATTTCTTCCCGTTCCCTTCATGGAATTTGAAGGCTCTCTTCTTCTCT	157
OY	273	TGAATGACTTTCATCCCTCTCTGTTTGTCTGAGATTTGGAGACATGTTGGATTTACTGGTGG	332
Db	158	TGAATGACTTTCATCCCTCTCTGTTTGTCTGAGATTTGGAGACATGTTGGATTTACTGGTGG	217
OY	333	AACCAAGCCCAACCACTACTCTAATATACACTTCTCTGACCAATGACCTGACTAGAGAG	392
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OY	393	TGATGAGAGAGTCTCTGCAAAAAGAGAGACCTCATCTCTCTCTACCATCCGGCTATCT	452
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OY	453	TCGCAACCCANGAAGCGCATTAACCTGGAACACATGGAAGAGAGCGCTGGTGATCCGGGCTC	512
Db	338	TCCCAACCCATGAACGCGATTAACCTGGAACACATGGAAGAGAGCGCTGGTGATCCGGGCTC	397
OY	513	TGGAGAACAGAGTGGGTATCTACT	572
Db	398	TGGAGAACAGAGTGGGTATCTACT	457
OY	573	TCACAACACTGGTGGCTTAAAGGCGTTGGAGCTTGTACTCTCCAGGCCCATCATCTCTTCCA	632
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OY	633	AAGCTCCCACTACCTTACAGAGGAAACACCGATGATGAATTCAGCTTACATCACCC	692
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OY	753	TTTCTGCTAGAGACTGTATATGAGAAACAACACGGATTAATCTGAATTTGACTCAGAGG	812
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Db	878	ATATTGCGTTAGCCCTTGGGGTGGGGAGAACCTTAGACTCTCAAGTCAAAATC 930	
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BX386928			
LOCUS			
DEFINITION	BX386928 Homo sapiens NEUROBLASTOMA COR 25-NORMALIZED Homo sapiens		
ACCESSION	BX386928		
VERSION	BX386928.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 1006)	Ll.W.B., Gruber,C., Jeesee,J. and Polayes,D.	Full-length cDNA libraries and normalization	Unpublished	
Genoscope				
Genoscope - Centre National de Sequencage				
Bp 191 91006 EVRI cedex - France				
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr				
Library was constructed by Life Technologies, a division of				
Invitrogen. This sequence belongs to sequence cluster 1287.f For				
more information about this cluster, see				
http://www.genoscope.cns.fr/				
cgl-bin/cluster.cgi?seq=CSIDC001ZF80Plc1cluster-1287.f. Contact :				
Feng Liang Email : fliang@life.com URL :				
http://fulllength.invitrogen.com/invitrogen Corporation 1600				
Faraday Avenue Genoscope sequence ID : CSIDC001ZF80Pl.				
Location/Qualifiers				
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/note="1st strand cDNA was primed with a NotI-oligo(dT)				
primer. Five prime end enriched, double-strand cDNA was				
digested with Not I and cloned into the Not I and EcoR V				
sites of the pCMVSPORT 6 vector. Library was normalized."				
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Best Local Similarity	97.9%:	Pred. No. 9.8e-22:		
Matches	868:	Conservative 11:	Mismatches 7:	Indels 1:
				Gaps 14:
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DB	179	CCTGCGCGACACGACAGACAGCAGCAGTGTGGAGAGGGGCTCTGACTCAGACTTAACG	238	
QY	121	CTGTGTCTGTGTGTTTCTACTGTCTCTGGAAAAGCCGTGAGTGGCACTGAATGAGCA	180	
DB	239	CTGTGTCTGTGTGTTTCTACTGTCTCTGGAAAAGCCGTGAGTGGCACTGAATGAGCA	298	
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DB	299	TGATGAGAGCCCCAGACAGAGTCCGGTTGTGATTCCTGATCTGCAATTCCTTCCGTTTC	358	
QY	241	CTTCATGATTTGAAGGCTCTCTCTTCTCTTCTTGAATGACTTTGATCCCTCTCCGTTTC	300	
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QY	301	TGAGAGTTGGGCAATGTTGATTACTGGTGGAGAACCCACCACTACTGTAAATAC	360	
DB	419	TGAGAGTTGGGCAATGTTGATTACTGGTGGAGAACCCACCACTACTGTAAATAC	478	
QY	361	ACTCTTCTGACCAATGACCTGACGAGGAATGATGAGAGAGGTGCTGCAAAAAGAGC	420	
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QY	421	AGACGCAATCTCTCTACATCCGCTATCTCTTCCGACCAAGAGCGATACCTGGA	480	
DB	539	AGACGCAATCTCTCTACATCCGCTATCTCTTCCGACCAAGAGCGATACCTGGA	598	
QY	481	CACATGAGAGAGCGCTGTGTATCCGGCTCTGGAGAACAGAGTGGATATCTACTCC	540	
DB	599	CACATGAGAGAGCGCTGTGTATCCGGCTCTGGAGAACAGAGTGGATATCTACTCC	658	
QY	541	TCATACGCTATGATGCTGCGCCCAAGGCGCTCAACAATGCTGCTAAAGGCTTGG	600	

Db 659 TCATACAGCCTATGATGCTGCGCCCGGCGTCAACAAGTGTGGCTAAAGGGCTTG 718
 QY 601 AGCTGTACCTCCAGGCCATACATCTCTCCAAAGCTCCCACTACCCCTACAGAGGAA 660
 Db 719 AGCTGTACCTCCAGGCCATACATCTCTCCAAAGCTCCCACTACCCCTACAGAGGAA 778
 QY 661 CCACGAGTAGAATTCACAGCTTACACACCCAGACCTGACAAAGATCTGTCAGT 720
 Db 779 CCACGAGTAGAATTCACAGCTTACACACCCAGACCTGACAAAGATCTGTCAGT 838
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 Db 839 KAAAGGAATTCAGAGGCTTCTGCTACTCTTTCTTCTGCTAGACCTGTAATGAGAGAA 898
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RESULT 11
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 LOCUS BX385101 Homo sapiens B CELLS (RAMOS CELL LINE) COR 25-NORMALIZED
 DEFINITION Homo sapiens cDNA clone CS0DL006YD12 3-PRIME, mRNA sequence.
 ACCESSION BX385101
 VERSION BX385101.1 GI:30453308
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 984)
 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 1287.f for
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DL006YD12&cluster=1287.f. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DL006YD12.6NP1.
 Location/Qualifiers
 1. 984

FEATURES
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DL006YD12"
 /cell_type="B CELLS (RAMOS CELL LINE) COR 25-NORMALIZED"
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 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 269 a 205 c 213 g 277 t 20 others
 ORIGIN

Query Match 55.1%; Score 855.6; DB 13; Length 984;
 Best Local Similarity 95.0%; Pred. No. 1.5e-220;
 Matches 927; Conservative 8; Mismatches 34; Indels 7; Gaps 5;

QY 555 ATGCTGCGCCCGGCGTCAACAACACTGTTGGCTAAAGGGCTTGAGACTTGTACTCCA 614

Db 970 WTGATSTGCCCGCGGCTCAACAACACTGTTGGCGMAAAG--ATTGAGCTTKACCTCCA 914
 QY 615 GGGCCATATATCTCTTCCAAAGCTCCCAACTACCTACAGAGGAAACCCAGATGAT 674
 Db 913 GGGCCATATAT-CTTCCAAAGCTCCCAACTACCTACAGAGGAAACCCAGATGAT 855
 QY 675 TCACGTTAATACACCCAGACCTGAGCAAGTCATGCTCAGTGAAGAAATGACG 734
 Db 854 TCACGTTAATACACCCAGACCTGAGCAAGTCATGCTCAGTGAAGAAATGACG 795
 QY 735 GTGTTCTGCTCACTTCTTTCTGCTAGAGCTGTAATGAGAAACAAACCGATTATC 794
 Db 794 GTGTTCTGCTCACTTCTTTCTGCTAGAGCTGTAATGAGAAACAAACCGATTATC 735
 QY 795 TGAATTTGCTCAGAAAGCTTTGATGACAGTGGTATTTT-TTTTCCGGAACAACA 853
 Db 734 TGAATTTGCTCAGAAAGCTTTGATGACAGTGGTATTTTCTTTCCGGAACAACA 675
 QY 854 CTTTATCAGAAAGCGAAATTCGTGCTAGAGAGCCCTTGTCTATACATCTGGAATG 913
 Db 674 CTTTATCAGAAAGCGAAATTCGTGCTAGAGAGCCCTTGTCTATACATCTGGAATG 615
 QY 914 GGAAGTTATGCACTGATGATGTCTCTCCCTGCGCAACATGATGATGATATAA 973
 Db 614 GGAAGTTATGCACTGATGATGTCTCTCCCTGCGCAACATGATGATGATATAA 555
 QY 974 AGACACCTAAACTATCATATTCGCTTAGCCCTGGGGTGGGGAACCTTAGAGTCT 1033
 Db 554 AGACACCTAAACTATCATATTCGCTTAGCCCTGGGGTGGGGAACCTTAGAGTCT 495
 QY 1034 CAAGTCAAAAGTGCGCCCTGTGTGCTGTGTGAGAGAGCGGTTCTCGAGGGTGTGAG 1093
 Db 494 CAAGTCAAAAGTGCGCCCTGTGTGCTGTGTGAGAGAGCGGTTCTCGAGGGTGTGAG 435
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 Db 434 GCTGACCTTTACCTCAGAGTGATGTCCCATCATGATCTTTGGATGCTGCTCCAA 375
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 Db 195 AGCTGATG-CCAACTTAATTTGTAACATGATGAGTGGAGCTGTGCTCCAGAGA 137
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 Db 136 GTGTCTTCGAGGTATCATCATTTCCGCTTTGTAATCTTATTCACCAATGTTCTATG 77
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 QY 1514 CTGAGAAAGTTGAAT 1529
 Db 16 AGDNNKKAATGMAAT 1

RESULT 12
 AK011670 1376 bp mRNA linear HTC 05-DEC-2002
 LOCUS AK011670 Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
 DEFINITION enriched library, clone:2610034I10 product:Nrg1 Interacting factor

ACCESSION AK011670
VERSION AK011670.1 GI:12847943
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE	1
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1995)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

QY 307 TTGGGACATGTTGGATTAGTGTGGAACCAAGCCACCACACTGTAAATACACTCTT 366
188 CTGGGACATGTGGATTACTGTGTGAGCAAGCCACCACCACTGTAAATACACTCTT 247
QY 367 CCTGACCAATGACCTGACCTGAGGAGAGTGTGAGAGGCTGTGCAAAAGAGGACAGCT 426
248 CCTGACCAATGACCTGACCTGAGGAGAGTGTGAGAGGCTGTGCAAAAGAGGACAGCT 307
QY 427 CATCTCTCTTACCATCCGCTATCTTCCGACCCATGAAAGCGCATACCTGGAACCATG 486
308 CATCTCTCTTACCATCCGCTATCTTCCGACCCATGAAAGCGCATACCTGGAACCATG 367
QY 487 GAAGGAGCGCTGTGTATCCGGCTCTGAGAAACAGAGTCGGATATCTCTCTCTATAC 546
368 GAAGGAGCTGTGTATCCGGCTCTGAGAAACAGAGTCGGATATCTCTCTCTATAC 427
QY 547 AACCTATGATGCTGGCCGCCCAAGGCGCTCAACAACCTGTTGGCTAAAGGCGCTTGAGACTTG 606
428 AACCTATGATGCTGGCCGCCCAAGGCGCTCAACAACCTGTTGGCTAAAGGCGCTTGAGACTTG 487
QY 607 TACCTCCAGGCCCATACATCTCTTCCAAAGCTCCCAACTACCCCTACAGAGGAAACACCG 666
488 CACTACCAAGGCCCATACATCTCTTCCAAAGCTCCCAACTACCCCTACAGAGGAAACACCG 547
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548 AGTAGAATTCAAGCTTAATACACCAACCAAGCTGGAACAGTCATCTGTGAGTAAAG 607
QY 727 AATGAGCGTGTGTGTCTGCTACTCTTCTTCTGCTAGAGCTGATGATGAGAAACAAACAG 786
608 GGTGGAATGTCTGTCTGCTACTCTTCTTCTGCTAGAGCTGATGATGAGAAACAAACAG 667
QY 787 GATTATCTGAATTGCTACTCAGAAAGCTTGTGATGAGTGTGATGATGATGATGATGATGAT 846
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QY 907 TGGAAATGGAGGTTATGACACACTGATGATGATGATGATGATGATGATGATGATGATGAT 966
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908 AAGAGCTCAAGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 967
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Db

RESULT 13
B0859307
LOCUS B0859307 929 bp mRNA linear EST 16-OCT-2002

DEFINITION
AGENCOURT_10422791 NIH_MGC_109 Homo sapiens cDNA clone
IMAGE:6650148.5', mRNA sequence.
B0859307
VERSION
B0859307.1 GI:24044299
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
NIH-MGC <http://mgi.nhl.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-femail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2894 row: 0 column: 12
High quality sequence stop: 754.
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XhoI; cDNA made by using 40-45 priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT
251 a 212 c 218 g 247 t 1 others
ORIGIN
Query Match 54.7%; Score 850.2; DB 13; Length 929;
Best Local Similarity 96.0%; Pred. No. 4.3e-219;
Matches 893; Conservative 0; Mismatches 34; Indels 3; Gaps 2;
QY 491 GAGCGGCTGGTATCCGGGCTCTGGAACAGAGGCTGATCTCTCTCTACAGCC 550
Db 1 GAGCGGCTGGTATCCGGGCTCTGGAACAGAGGCTGATCTCTCTCTCTACAGCC 60
QY 551 TATGATGCTGCGGCCCGAGGCGTCAACAACTGTTGGCTTAAGGCTTGGAGCTTAC 610
Db 1 TATGATGCTGCGGCCCGAGGCGTCAACAACTGTTGGCTTAAGGCTTGGAGCTTAC 120
QY 611 TCCAGGCCATACATCTTCCAAAGCTCCCACTACCTCAGAGGAAACCAAGTA 670
Db 121 TCCAGGCCATACATCTTCCAAAGCTCCCACTACCTCAGAGGAAACCAAGTA 180
QY 671 GAATTCAGCTTAACATCAACCCCAAGACCTGGAAGTATGCTCAGAGGAAGGAAT 730
Db 181 GAATTCAGCTTAACATCAACCCCAAGACCTGGAAGTATGCTCAGAGGAAGGAAT 240
QY 731 GAGCGGCTTCTGCTACTCTTCTTCTGCTAGAGCTGTAATAGGAACAAACAGGATT 790
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QY 791 AATCTGAATTTACTCAGAAAGGCTTGAATGAGTGTATGATTTCTTCCGGAACAA 850
Db 301 AATCTGAATTTACTCAGAAAGGCTTGAATGAGTGTATGATTTCTTCCGGAACAA 360
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Db	Accession	Source	Length	EST	EST Date
Db	361	CAACCTTATACGAAAGACGGAATATCTGTCACCTGGAGAAAGCCTTGCTTCACATACAGTGA	970		
Db	911	ATGGAGCGGTATATGACACACTGGATGAAATCTGTCTCCCTGGACACCATGATGATGATGA	970		
Db	421	ATGGAGCGGTATATGACACACTGGATGAAATCTGTCTCCCTGGACACCATGATGATGATGA	480		
Db	971	AAAGACACCTAAACCTATCTCATATTCCTAGACCCCTTGGGGGGGGAAACCTTGGAG	1030		
Db	481	AAAGACACCTAAACCTATCTCATATTCCTAGACCCCTTGGGGGGGGAAACCTTGGAG	540		
Db	1031	TCTCAGTCAAAAGTCTGTGGCCCTGTGTCTGGTCTGTGGAGACAGCTTCACAGAGTGT	1090		
Db	541	TCTCAGTCAAAAGTCTGTGGCCCTGTGTCTGGTCTGTGGAGACAGCTTCACAGAGTGT	600		
Db	1091	GAGCGTACCTTTACCTTCACAGGTGAGATGTCCATCATGATTTGGATGATGCTGCTTC	1150		
Db	601	GAGCGTACCTTTACCTTCACAGGTGAGATGTCCATCATGATTTGGATGATGCTGCTTC	660		
Db	1151	CAAGGAATAAATGTCATCTCTGTGGAACACAGCAACACTGAACAGAGCTTCTTCTTGAC	1210		
Db	661	CAAGGAATAAATGTCATCTCTGTGGAACACAGCAACACTGAACAGAGCTTCTTCTTGAC	720		
Db	1211	CTTGAGATATGCTGAGATCTCCTACCTGGAGAAATTAATATATTCCTTCAGAGCT	1270		
Db	721	CTTGAGATATGCTGAGATCTCCTACCTGGAGAAATTAATATATTCCTTCAGAGACT	780		
Db	1271	GACAGGAGCCCTCTTCAGGTGTAAATTTGAGAAACATCAGATTAACATCTTCTACAA	1330		
Db	781	GACAGGAGCCCTCTTCAGGTGTAAATTTGAGAAACATCAGATTAACATCTTCTACAA	839		
Db	1331	ATCAGCTGTGATGCCCACTTAATTTGTAAATGATGATGATGATGATGATGATGATGATG	1388		
Db	840	ATCAGCTGTGATGCCCACTTAATTTGTAAATGATGATGATGATGATGATGATGATGATG	899		
Db	1389	AGAGATGTCTTCAGGAGTATCATCATTTTC 1418			
Db	900	CCAGAAAGTGTCTTCAGGATTAATCTTTC 929			
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LOCUS	B0927763	985 bp	mRNA	linear	EST 20-AUG-2002
DEFINITION	AGENCOURT-8774801 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6370367				
ACCESSION	B0927763				
VERSION	B0927763.1	GI:22342794			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1 (bases 1 to 985)				
JOURNAL	NIH-MGC http://mgi.nci.nih.gov/				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished				
	Contact: Robert Strausberg, Ph.D.				
	Email: cga@pds.fda.gov				
	Tissue Procurement: DCRD/DTP/Gasdar				
	CDNA Library Preparation: Robin Laboratory				
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)				
	DNA Sequencing by: Agencourt Bioscience Corporation				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LNL at:				
	http://image.llnl.gov				
	Plate: L1CM2542 row: m column: 24				
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	High quality sequence stop: 737.				
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 LOCUS AL521919 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
 DEFINITION cDNA clone CSDB0037P14 3-PRIME, mRNA sequence.
 ACCESSION AL521919
 VERSION AL521919.2 GI:31040193
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 961)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 On Feb. 13, 2001 this sequence version replaced gi:12785412.
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by life technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 1287.f For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CSDB003DH07NP1&cluster=1287.f. Contact :
 Feng Liang Email: fliang@life.technologies.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CSDB003DH07NP1.
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 215 a 209 c 237 g 269 t 31 others
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 Query Match 54.6%; Score 847.4; DB 9; Length 961;
 Best Local Similarity 92.0%; Pred. No. 2,5e-218;
 Matches 885; Conservative 22; Mismatches 53; Indels 2; Gaps 2;
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 QY 619 CATACATCTCTCCAAAGCTCCCACTACCTACAGAGGAAACACCGAGTGAATTCAA 678
 Db 900 CATACATCTCTCCAAAGCTCCCACTACCTACAGAGGAAACACCGAGTGAATTCAA 841
 QY 679 CGTTAACTACACCAAGACCTGGACAAAGTCAATGCTGAGTGAAGGAATGAGCGTGT 738
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 Db 780 TTCTGTCACTCTTTTCTGTAGAGCTGTATAGAGAAACAACGAGTAACTGAA 721
 QY 799 TTGTACTGAAAGGCTTATGAGGTAGATTCTTCCCGGAACAACACTTAA 858
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Db 720 TTGTACTGAAAGGCTTTGATGACAGGTGTAGATTTCTTCCGGAAACAACACTTAA 661
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 Db 660 TCAGAAAGCGGAATTTGTCTACCTGAGAGAGCCCTTGTCTTACACTGGAATGGAGC 601
 QY 919 GTTATGACACCTGATGATATCTGTCTCCCTGGCAACCATGATGATGATTAATAAGCA 978
 Db 600 GTTATGACACCTGATGATGATATCTGTCTCCCTGGCAACCATGATGATGATTAATAAGCA 541
 QY 979 CCTAAACATATCTATATTCGCTTACCTGAGGCTGGGGGAGAAACCTTAGAGTCAAGT 1038
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 Db 480 CAAAGTCTGGCCCTGTGTGCTGTGTGAGAGACCGCTTGTGACAGGCTGTGAGGCTGA 421
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 QY 1519 AA 1520
 Db 2 AA 1

Search completed: August 23, 2003, 14:21:46
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